

SEQUENCE LISTING

<110> William Gaarde
Andrew T. Watt

<120> ANTISENSE MODULATION OF CONNECTIVE TISSUE GROWTH FACTOR EXPRESSION

<130> RTS-0274

<160> 153

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<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Antisense Oligonucleotide

<400> 1

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<210> 2

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<223> Antisense Oligonucleotide

<400> 2

10006191.12.001

atgcattctg cccccaagga

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<211> 2075

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (130) ... (1179)

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 gtgccaacc atg acc gcc gcc agt atg ggc ccc gtc cgc gtc gcc ttc gtg 171

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val

1

5

10

gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc ggc cag aac tgc agc 219
 Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser
 15 20 25 30

ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg cgc tgc ccg gcg ggc 267
 Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly
 35 40 45

gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc cgc gtc tgc gcc aag 315
 Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys
 50 55 60

cag ctg ggc gag ctg tgc acc gag cgc gac ccc tgc gac ccg cac aag 363
 Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys
 65 70 75

ggc ctc ttc tgt gac ttc ggc tcc ccg gcc aac cgc aag atc ggc gtg 411
 Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val
 80 85 90

10006191.1.2.1001

tgc acc gcc aaa gat ggt gct ccc tgc atc ttc ggt ggt acg gtg tac 459
 Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr
 95 100 105 110

cgc agc gga gag tcc ttc cag agc agc tgc aag tac cag tgc acg tgc 507
 Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys
 115 120 125

ctg gac ggg gcg gtg ggc tgc atg ccc ctg tgc agc atg gac gtt cgt 555
 Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg
 130 135 140

ctg ccc agc cct gac tgc ccc ttc ccg agg agg gtc aag ctg ccc ggg 603
 Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly
 145 150 155

aaa tgc tgc gag gag tgg gtg tgt gac gag ccc aag gac caa acc gtg 651
 Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val
 160 165 170

gtt ggg cct gcc ctc gcg gct tac cga ctg gaa gac acg ttt ggc cca 699
 Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro
 175 180 185 190

gac cca act atg att aga gcc aac tgc ctg gtc cag acc aca gag tgg 747
 Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp
 195 200 205

agc gcc tgt tcc aag acc tgt ggg atg ggc atc tcc acc cgg gtt acc 795
 Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr
 210 215 220

aat gac aac gcc tcc tgc agg cta gag aag cag agc cgc ctg tgc atg 843
 Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met
 225 230 235

gtc agg cct tgc gaa gct gac ctg gaa gag aac att aag aag ggc aaa 891

10006491.1E1001

Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys
 240 245 250

aag tgc atc cgt act ccc aaa atc tcc aag cct atc aag ttt gag ctt 939
 Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu
 255 260 265 270

tct ggc tgc acc agc atg aag aca tac cga gct aaa ttc tgt gga gta 987
 Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val
 275 280 285

tgt acc gac ggc cga tgc tgc acc ccc cac aga acc acc acc ctg ccg 1035
 Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro
 290 295 300

gtg gag ttc aag tgc cct gac ggc gag gtc atg aag aag aac atg atg 1083
 Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met
 305 310 315

ttc atc aag acc tgt gcc tgc cat tac aac tgt ccc gga gac aat gac 1131
 Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp
 320 325 330

atc ttt gaa tcg ctg tac tac agg aag atg tac gga gac atg gca tga 1179
 Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala *
 335 340 345

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ttgtttgtgc ctttttattt ttgttttttaa tgctttgata tttcaatgtt agcctcaatt 1899
tctgaacacc ataggtagaa tgtaaagctt gtctgatcgt tcaaagcatg aaatggatac 1959
ttatatggaa attctgctca gatagaatga cagtccgtca aaacagattg ttgcaaagg 2019
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<400> 4

acaagggcct cttctgtgac tt

22

<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 5

ggtacaccgt accaccgaag at

22

<210> 6

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

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<223> PCR Probe

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tgtgcaccgc caaagatggt gct

23

<210> 7

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 7

gaaggtgaag gtcggagtc

19

<210> 8

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primer

<400> 8

gaagatggtg atgggatttc

20

<210> 9

<211> 20

<212> DNA

<213> Artificial Sequence

10006191.12.001

<220>

<223> PCR Probe

<400> 9

caagcttccc gttctcagcc

20

<210> 10

<211> 2334

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (206)...(1252)

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 ctccgcccct gtccgaatcc aggetccggc cgcgcctctc gtcgcctctg caccctgctg 180
 tgcacacctc taccgcgtcc cgatc atg ctc gcc tcc gtc gca ggt ccc atc 232

Met Leu Ala Ser Val Ala Gly Pro Ile

1

5

agc ctc gcc ttg gtg ctc ctc gcc ctc tgc acc cgg cct gct acg ggc 280
 Ser Leu Ala Leu Val Leu Leu Ala Leu Cys Thr Arg Pro Ala Thr Gly

10

15

20

25

cag gac tgc agc gcg caa tgt cag tgc gca gcc gaa gca gcg ccg cac 328
 Gln Asp Cys Ser Ala Gln Cys Gln Cys Ala Ala Glu Ala Ala Pro His

30

35

40

tgc ccc gcc ggc gtg agc ctg gtg ctg gac ggc tgc ggc tgc tgc cgc 376
 Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg

45

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gtc tgc gcc aag cag ctg gga gaa ctg tgt acg gag cgt gac ccc tgc 424
 Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys
 60 65 70

gac cca cac aag ggc ctc ttc tgc gat ttc ggc tcc ccc gcc aac cgc 472
 Asp Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg
 75 80 85

aag atc gga gtg tgc act gcc aaa gat ggt gca ccc tgt gtc ttc ggt 520
 Lys Ile Gly Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Val Phe Gly
 90 95 100 105

ggg tcg gtg tac cgc agc ggt gag tcc ttc caa agc agc tgc aaa tac 568
 Gly Ser Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr
 110 115 120

caa tgc act tgc ctg gat ggg gcc gtg ggc tgc gtg ccc ctg tgc agc 616
 Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Val Pro Leu Cys Ser
 125 130 135

atg gac gtg cgc ctg ccc agc cct gac tgc ccc ttc ccg aga agg gtc 664
 Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val
 140 145 150

aag ctg cct ggg aaa tgc tgc gag gag tgg gtg tgt gac gag ccc aag 712
 Lys Leu Pro Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys
 155 160 165

gac cgc aca gca gtt ggc cct gcc cta gct gcc tac cga ctg gaa gac 760
 Asp Arg Thr Ala Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp
 170 175 180 185

aca ttt ggc cca gac cca act atg atg cga gcc aac tgc ctg gtc cag 808
 Thr Phe Gly Pro Asp Pro Thr Met Met Arg Ala Asn Cys Leu Val Gln
 190 195 200

acc aca gag tgg agc gcc tgt tct aag acc tgt ggg atg ggc atc tcc 856
 Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser

10006191-121001

205	210	215	
acc cga gtt acc aat gac aat acc ttc tgc aga ctt gag aag cag agt			904
Thr Arg Val Thr Asn Asp Asn Thr Phe Cys Arg Leu Glu Lys Gln Ser			
220	225	230	
cgc ctc tgc atg gtc agg ccc tgc gaa gct gac ctg gag gaa aac att			952
Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile			
235	240	245	
aag aag ggc aaa aag tgc atc cgg aca cct aaa atc gcc aag cct gtc			1000
Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ala Lys Pro Val			
250	255	260	265
aag ttt gag ctt tct ggc tgc acc agt gtg aag aca tac agg gct aag			1048
Lys Phe Glu Leu Ser Gly Cys Thr Ser Val Lys Thr Tyr Arg Ala Lys			
270	275	280	
ttc tgc ggg gtg tgc aca gac ggc cgc tgc tgc aca ccg cac aga acc			1096
Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr			
285	290	295	
acc act ctg cca gtg gag ttc aaa tgc ccc gat ggc gag atc atg aaa			1144
Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Ile Met Lys			
300	305	310	
aag aat atg atg ttc atc aag acc tgt gcc tgc cat tac aac tgt cct			1192
Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro			
315	320	325	
ggg gac aat gac atc ttt gag tcc ctg tac tac agg aag atg tac gga			1240
Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly			
330	335	340	345
gac atg gcg taa agccaggaag taaggacac gaactcatta gactataact			1292
Asp Met Ala *			

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tgaactgagt tgcattctcat tttcttctgt aaaaacaatt acagtagcac attaatTTAA 1352
 atctgtgttt ttaactaccg tgggaggaac tatcccacca aagtgagaac gttatgtcat 1412
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 gcttctttga ttatgactgg tttgggggtg ggggcagttt atttggtgag agtgtgacca 2252
 aaagttacat gtttgcacct ttctagttga aaataaagta tatatatatt ttttatatga 2312
 aaaaaaaaaa aaaaaaaaaa aa 2334

<210> 11

<211> 21

<212> DNA

<213> Artificial Sequence

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<400> 11

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21

<210> 12

<211> 15

<212> DNA

<213> Artificial Sequence

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<223> PCR Primer

<400> 12

gccccccacc ccaaa

15

<210> 13

<211> 31

<212> DNA

<213> Artificial Sequence

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<223> PCR Probe

<400> 13

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31

<210> 14

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> PCR Primer

<400> 14

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20

<210> 15

<211> 20

<212> DNA

<213> Artificial Sequence

10006191 "121001

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<211> 27

<212> DNA

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<220>

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27

<210> 17

<211> 2312

<212> DNA

<213> Homo sapiens

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<222> (146)...(1195)

<400> 17

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ctccgctccg cccgcagtgc caacc atg acc gcc gcc agt atg ggc ccc gtc 172

Met Thr Ala Ala Ser Met Gly Pro Val

cgc gtc gcc ttc gtg gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc 220
 Arg Val Ala Phe Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val
 10 15 20 25

ggc cag aac tgc agc ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg 268
 Gly Gln Asn Cys Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro
 30 35 40

cgc tgc ccg gcg ggc gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc 316
 Arg Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys
 45 50 55

cgc gtc tgc gcc aag cag ctg ggc gag ctg tgc acc gag cgc gac ccc 364
 Arg Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro
 60 65 70

tgc gac ccg cac aag ggc ctc ttc tgt gac ttc ggc tcc ccg gcc aac 412
 Cys Asp Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn
 75 80 85

cgc aag atc ggc gtg tgc acc gcc aaa gat ggt gct ccc tgc atc ttc 460
 Arg Lys Ile Gly Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe
 90 95 100 105

ggt ggt acg gtg tac cgc agc gga gag tcc ttc cag agc agc tgc aag 508
 Gly Gly Thr Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys
 110 115 120

tac cag tgc acg tgc ctg gac ggg gcg gtg ggc tgc atg ccc ctg tgc 556
 Tyr Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys
 125 130 135

agc atg gac gtt cgt ctg ccc agc cct gac tgc ccc ttc ccg agg agg 604
 Ser Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg
 140 145 150

gtc aag ctg ccc ggg aaa tgc tgc gag gag tgg gtg tgt gac gag ccc 652

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Val Lys Leu Pro Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro
 155 160 165

aag gac caa acc gtg gtt ggg cct gcc ctc gcg gct tac cga ctg gaa 700
 Lys Asp Gln Thr Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu
 170 175 180 185

gac acg ttt ggc cca gac cca act atg att aga gcc aac tgc ctg gtc 748
 Asp Thr Phe Gly Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val
 190 195 200

cag acc aca gag tgg agc gcc tgt tcc aag acc tgt ggg atg ggc atc 796
 Gln Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile
 205 210 215

tcc acc cgg gtt acc aat gac aac gcc tcc tgc agg cta gag aag cag 844
 Ser Thr Arg Val Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln
 220 225 230

agc cgc ctg tgc atg gtc agg cct tgc gaa gct gac ctg gaa gag aac 892
 Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn
 235 240 245

att aag aag ggc aaa aag tgc atc cgt act ccc aaa atc tcc aag cct 940
 Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro
 250 255 260 265

atc aag ttt gag ctt tct ggc tgc acc agc atg aag aca tac cga gct 988
 Ile Lys Phe Glu Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala
 270 275 280

aaa ttc tgt gga gta tgt acc gac ggc cga tgc tgc acc ccc cac aga 1036
 Lys Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg
 285 290 295

acc acc acc ctg ccg gtg gag ttc aag tgc cct gac ggc gag gtc atg 1084
 Thr Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met
 300 305 310

10006191 "121001
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aag aag aac atg atg ttc atc aag acc tgt gcc tgc cat tac aac tgt 1132
Lys Lys Asn Met Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys
315 320 325

ccc gga gac aat gac atc ttt gaa tcg ctg tac tac agg aag atg tac 1180
Pro Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr
330 335 340 345

gga gac atg gca tga agccagagag tgagagacat taactcatta gactggaact 1235
Gly Asp Met Ala *

tgaactgatt cacatctcat ttttccgtaa aaatgatttc agtagcaciaa gttattttaa 1295
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ctctatatag ctgatcagtt ttttcacctg gaagcatttg tttctacttt gatatgactg 2195
tttttcggac agtttatattg ttgagagtgt gaccaaaagt tacatgtttg cacctttcta 2255
gttgaaaata aagtatatct tttctaaaaa aaaaaaaaaa cgacagcaac ggaattc 2312

<210> 18

<211> 2078

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (131)...(1180)

<400> 18

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 agtgccaacc atg acc gcc gcc agt atg ggc ccc gtc cgc gtc gcc ttc 169

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe

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10

gtg gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc ggc cag aac tgc 217
 Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys

15

20

25

agc ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg cgc tgc ccg gcg 265
 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala
 30 35 40 45

ggc gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc cgc gtc tgc gcc 313
 Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala

50

55

60

aag cag ctg ggc gag ctg tgc acc gag cgc gac cca tgc gac ccg cac 361
 Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His

65

70

75

aag ggc cta ttc tgt cac ttc ggc tcc ccg gcc aac cgc aag atc ggc 409
 Lys Gly Leu Phe Cys His Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly

80

85

90

gtg tgc acc gcc aaa gat ggt gct ccc tgc atc ttc ggt ggt acg gtg 457
 Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val

95

100

105

tac cgc agc gga gag tcc ttc cag agc agc tgc aag tac cag tgc acg 505
 Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr

110

115

120

125

10006191.121001

tgc ctg gac ggg gcg gtg ggc tgc atg ccc ctg tgc agc atg gac gtt 553
 Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val
 130 135 140

cgt ctg ccc agc cct gac tgc ccc ttc ccg agg agg gtc aag ctg ccc 601
 Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro
 145 150 155

ggg aaa tgc tgc gag gag tgg gtg tgt gac gag ccc aag gac caa acc 649
 Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr
 160 165 170

gtg gtt ggg cct gcc ctc gcg gct tac cga ctg gaa gac acg ttt ggc 697
 Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly
 175 180 185

cca gac cca act atg att aga gcc aac tgc ctg gtc cag acc aca gag 745
 Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu
 190 195 200 205

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 Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val
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acc aat gac aac gcc tcc tgc agg cta gag aag cag agc cgc ctg tgc 841
 Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys
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atg gtc agg cct tgc gaa gct gac ctg gaa gag aac att aag aag ggc 889
 Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly
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aaa aag tgc atc cgt act ccc aaa atc tcc aag cct atc aag ttt gag 937
 Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu
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ctt tct ggc tgc acc agc atg aag aca tac cga gct aaa ttc tgt gga 985

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Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly
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 Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu
 290 295 300

 ccg gtg gag ttc aag tgc cct gac ggc gag gtc atg aag aag aac atg 1081
 Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met
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 Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn
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 Met Thr Ala Ala Ser Met Gly Pro Val Arg
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gtc gcc ttc gtg gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc ggc 220
 Val Ala Phe Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly
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 Gln Asn Cys Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg
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 Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg
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gtc tgc gcc aag cag ctg ggc gag ctg tgc acc gag cgc gac cca tgc 364
 Val Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys
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gac ccg cac aag ggc cta ttc tgt cac ttc ggc tcc ccg gcc aac cgc 412
 Asp Pro His Lys Gly Leu Phe Cys His Phe Gly Ser Pro Ala Asn Arg
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 Lys Ile Gly Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly
 95 100 105

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 Gly Thr Val Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr
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cag tgc acg tgc ctg gac ggg gcg gtg ggc tgc atg ccc ctg tgc agc 556
 Gln Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser
 125 130 135

atg gac gtt cgt ctg ccc agc cct gac tgc ccc ttc ccg agg agg gtc 604
 Met Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val
 140 145 150

aag ctg ccc ggg aaa tgc tgc gag gag tgg gtg tgt gac gag ccc aag 652
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 155 160 165 170

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 Thr Phe Gly Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln
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 Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser
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acc cgg gtt acc aat gac aac gcc tcc tgc agg cta gag aag cag agc 844
 Thr Arg Val Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser
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cgc ctg tgc atg gtc agg cct tgc gaa gct gac ctg gaa gag aac att 892
 Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile

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 270 275 280

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 Phe Cys Gly Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr
 285 290 295

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 Thr Thr Leu Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys
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 315 320 325 330

 gga gac aat gac atc ttt gaa tcg ctg tac tac agg aag atg tac gga 1180
 Gly Asp Asn Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly
 335 340 345

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 Met Leu Ala Ser Val Ala Gly Pro Ile Ser
 1 5 10

ctc gcc ttg gtg ctc ctc gcc ctc tgc acc cgg cct gct acg ggc cag 281
 Leu Ala Leu Val Leu Leu Ala Leu Cys Thr Arg Pro Ala Thr Gly Gln
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 Asp Cys Ser Ala Gln Cys Gln Cys Ala Ala Glu Ala Ala Pro His Cys
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ccc gcc ggc gtg agc ctg gtg ctg gac ggc tgc ggc tgc tgc cgc gtc 377
 Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val
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tgc gcc aag cag ctg gga gaa ctg tgt acg gag cgt gac ccc tgc gac 425
 Cys Ala Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp
 60 65 70

cca cac aag ggc ctc ttc tgc gat ttc ggc tcc ccc gcc aac cgc aag 473
 Pro His Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys
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att gga gtg tgc act gcc aaa gat ggt gca ccc tgt gtc ttc ggt ggg 521

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 Cys Thr Cys Leu Asp Gly Ala Val Gly Cys Val Pro Leu Cys Ser Met
 125 130 135

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 Asp Val Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys
 140 145 150

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 Phe Gly Pro Asp Pro Thr Met Met Arg Ala Asn Cys Leu Val Gln Thr
 190 195 200

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 205 210 215

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 Arg Val Thr Asn Asp Asn Thr Phe Cys Arg Leu Glu Lys Gln Ser Arg
 220 225 230

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